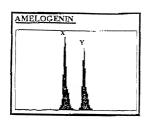
# 09910183.078001

## FIGURE 1

0

									The second secon		
loci	allelic designat ion	size (bp)	loci	allelic designat ion	size (bp)	loci	allelic designat lon n	size (bp)	loci	allelic designa tion n	size (bp)
THOI	4	150	D8	7	157	D18	88	266	FGA (LMW)	16.1	173
	5	154		8	161		6	270		17	176
	9	158		6	165		10	274		18	180
	7	162		10	169		11	278		19	184
	8	166		11	173		1.2	282		20	188
	6	170		1.2	177		13	286		21	192
	6.3	173		13	181		14	290		22	196
	10	174		14	185		1.5	294		23	200
	111	178		15	189		16	298		24	204
	13.3	189		16	193		1.7	302		25	208
D2.1	53	203		1.7	197		1.8	306		26	212
	54	205		1.8	201		19	310		27	216
	56	209		19	205		2.0	314		28	220
	57	211	VWA	1.0	122		21	318		29	224
	59	215		11	126		22	322		30	228
	61	219		12	130		23	326		30.2	230
	63	223		13	134		24	330		31.2	234
	65	227		14	138		25	334		32.2	238
	67	231		1.5	142		26	338		33.2	242

0.9	_	223	16	146		27	342	34.2	246
2 6		237	17	150	AMELO	×	105	42.2	278
72	,	241	18	154		Y	111	42.3	282
7.4		245	19	158				44.2	286
1	75	247	20	162				45.2	290
1	77	251	2.1	166				46.2	294
1	10	255						47.2	298
	, ,	200						 48.2	302
0	4	66.7						50.2	310



()

Fig 2a

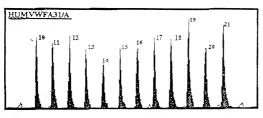


Fig 2b

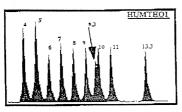


Fig 2c

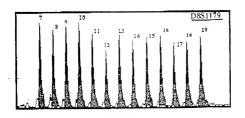
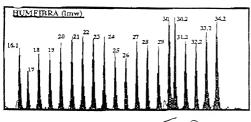


Fig 2d



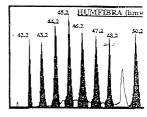
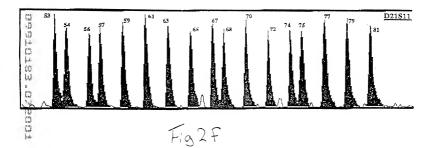


Fig2e



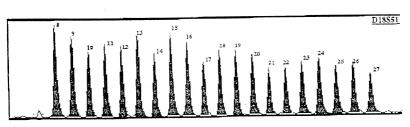


Fig 2g

#### HUMVWAF31/A sequences

- 10 TCTA TCTG TCTA (TCTG)4 (TCTA);
- 12 TCTA (TCTG)4 (TCTA)2

13 (TCTA)<sub>2</sub> (TCTG)<sub>3</sub> (TCTA)<sub>5</sub> TCCA (TCTA)<sub>5</sub> (TCCA)<sub>5</sub> T (Note also that the 13 allele has a typical 3' flanking sequence (highlighted). The usual sequence is TCCA TCTA T.)

### Fig 3a

#### HUMTHO1 sequences

13.3 (TCAT), CAT (TCAT), TCGT TCAT

Fig3b

#### D8S1179 sequences

- 7 (TCTA) ,;
- 19 (TCTA) 2 TCTG (TCTA) 16;

Fig 3c

#### HUMFIBRA(FGA) Repeat Sequences

- 16.1 (TTTC), TTTT TTCT (CTTT), T (CTTT), CTCC (TTCC)2.
- 27 (TTTC)<sub>3</sub> TTTT TTCT (CTTT)<sub>15</sub> CCTT (CTTT)<sub>5</sub> CTCC (TTCC)<sub>2</sub>.
- 30 (TTTC)<sub>3</sub> TTTT TTCT (CTTT)<sub>16</sub> CCTT (CTTT)<sub>5</sub> CTCC (TTCC)<sub>2</sub>.
- 31.2 (TTTC), TTTT TT (CTTT), (CTTC), (CTTT), CTCC (TTCC),
- 32.2 (TTTC),4 TTTT TT (CTTT),16 (CTTC),5 (CTTT),3 CTCC (TTCC),4
- 33.2 (TTTC)<sub>4</sub> TTTT TT (CTTT)<sub>17</sub> (CTTC)<sub>3</sub> (CTTT)<sub>3</sub> CTCC (TTCC)<sub>4</sub>
- 42.2 (TTTC), TTTT TT (CTTT): (CTGT), (CTTT): (CTTC), (CTTC), (CTTT); CTCC (TTCC) ,
- 43.2 (TTTC), TTTT TT (CTTT): (CTGT); (CTTT):; (CTTC), (CTTT); CTCC (TTCC),
- 44.2 (ITTC), TITT IT (CITT), (CIGT), (CITT), (CTTC), (CITT), CTCC (TICC),
- 45.2 (TTTC), TTTT TT (CTTT), (CTGT), (CTGT), (CTTT), (CTTC), (CTTT), CTCC (TTCC),
  - 47.2 (TTTC), TTTT TT (CTTT), (CTGT), (CTTT), (CTTC), (CTTT), CTCC (TTCC),
  - 48.2 (TTTC), TTTT TT (CTTT), (CTGT), (CTTT), (CTTC), (CTTC), (CTTT),

Fig. 3d

#### D21S11\_alleles

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- 53 (TCTA), (TCTG), (TCTA), TA (TCTA), TCA (TCTA); TCCATA (TCTA)
- 54 (TCTA)<sub>5</sub> (TCTG)<sub>6</sub> (TCTA)<sub>3</sub> TCA (TCTA)<sub>2</sub> TCCATA (TCTA)<sub>9</sub> TCGTCT
- 56 (TCTA)<sub>5</sub> (TCTG)<sub>6</sub> (TCTA)<sub>3</sub> TCA (TCTA)<sub>1</sub> TCCATA (TCTA)<sub>1</sub> TCGTCT
- 57 (TCTA), (TCTG), (TCTA), TA (TCTA), TCA (TCTA), TCCATA (TCTA), TCGTCT
- 59 (TCTA)<sub>5</sub> (TCTG)<sub>5</sub> (TCTA)<sub>5</sub> TA (TCTA)<sub>7</sub> TCA (TCTA)<sub>1</sub> TCCATA (TCTA)
  7 TCGTCT
- 61 (TCTA), (TCTG), (TCTA), TA (TCTA), TCA (TCTA), TCCATA (TCTA)  $_{10}$  TCGTCT
- $^{63}$  (TCTA), (TCTG), (TCTA), TA (TCTA), TCA (TCTA), TCCATA (TCTA) ITCGTCT
- 65 (TCTA)6 (TCTG)5 (TCTA)5 TA (TCTA)5 TCA (TCTA)2 TCCATA (TCTA)
  11 TCGTCT
- 67 (TCTA)5 (TCTG)6 (TCTA)5 TA (TCTA)5 TCA (TCTA)2 TCCATA (TCTA)22 TCGTCT
- 68 (TCTA)<sub>5</sub> (TCTG)<sub>6</sub> (TCTA)<sub>5</sub> TA (TCTA)<sub>5</sub> TCA (TCTA)<sub>2</sub> TCCATA (TCTA)<sub>11</sub> TA TCTA TCGTCT.
- 70 (TCTA) $_5$  (TCTG) $_6$  (TCTA) $_5$  TA (TCTA) $_5$  TCA (TCTA) $_2$  TCCATA (TCTA) $_2$  TA TCTA TCGTCT
- 72 (TCTA)<sub>5</sub> (TCTG)<sub>6</sub> (TCTA)<sub>3</sub> TA (TCTA)<sub>3</sub> TCA (TCTA)<sub>2</sub> TCCATA (TCTA)<sub>13</sub> TA TCTA TCGTCT
- 74 (TCTA) $_5$  (TCTG) $_6$  (TCTA) $_7$  TA (TCTA) $_7$  TCA (TCTA) $_7$  TCCATA (TCTA) $_7$  TATCTA TCGTCT
- 75 (TCTA) $_5$  (TCTA) $_5$  (TCTA) $_5$  TA (TCTA) $_7$  TCA (TCTA) $_7$  TCCATA (TCTA) $_7$  TCGTCT
- 77 (TCTA)  ${\rm u}$  (TCTG)5 (TCTA)3 TA (TCTA)5 TCA (TCTA)2 TCCATA (TCTA)22 TCGTCT
- 79 (TCTA) $_{11}$  (TCTG) $_{22}$  (TCTA) $_{23}$  TA (TCTA) $_{23}$  TCA (TCTA) $_{22}$  TCCATA (TCTA) $_{123}$  TCGTCT
- 81 (TCTA) $_5$  (TCTG) $_5$  (TCTA) $_5$  TA (TCTA) $_5$  TCA (TCTA) $_2$  TCCATA (TCTA) $_2$  TCGTCT

#### D18S51 sequences

8 (AGAA)6

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Fig3F

Fig3e